CRF Errors Corrected by the STIC Systems Branch **ENTERED**

Serial Number: 09/934,249

CRF Processing Date: 10/12/2001
Edited by:
Verified by: _____ (STIC star

#2

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically:
  _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____:

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
  _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
  _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included:

- [ ] Deleted extra, invalid, headings used by an applicant, specifically:
  _____

- [ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically:
  _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically:
  _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [✓] Other: *Seq 16 - inserted hard return* _____
  _____
  _____
  _____

RAW SEQUENCE LISTING   DATE: 10/17/2001
PATENT APPLICATION: US/09/934,249   TIME: 12:05:07

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10172001\I934249.raw

```
 4 <110> APPLICANT: Lee, Richard T.
 5         Landschulz, Katherine T.
 6         Turi, Thomas G.
 7         Thompson, John F.
 8         Kennedy, Scott P.
10 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
11         CARDIOVASCULAR CONDITIONS
13 <130> FILE REFERENCE: P0738/7001/ERP/KA
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C--> 15 **<140> CURRENT APPLICATION NUMBER: US/09/934,249**
C--> 15 **<141> CURRENT FILING DATE: 2001-08-21**
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15 <150> PRIOR APPLICATION NUMBER: US 60/227,159
16 <151> PRIOR FILING DATE: 2000-08-22
18 <160> NUMBER OF SEQ ID NOS: 17
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1321
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo Sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (413)...(1273)
31 <400> SEQUENCE: 1
32  cgaccgcggt ctcggagcga aacccgatct ccttggactt gaatgaggag gaggaggcgg      60
33  cggcggcggc ggcggcggag gcgctcggct ggggaaagct agcggcagag gctcagcccc     120
34  ggcggcagcg cgcgccccgc tgccagccca ttttccggac gccacccgcg ggcactgccg     180
35  acgcccccgg ggctgccgag gggaggccgg gggggcgcag cggagcgcgg tcccgcgcac     240
36  tgagccccgc ggcgccccgg gaacttggcg gcgacccgag cccggcgagc cggggcgcgc     300
37  ctcccccgcc gcgcgcctcc tgcatgcggg gccccagctc cgggcgccgg ccggagcccc     360
38  ccccggccgc ccccgagccc cccgcgcccc gcgccgcgcc gccgcgccgt cc atg cac     418
39                                                          Met His
40                                                           1
42  cgc ttg atg ggg gtc aac agc acc gcc gcc gcc gcc gcc ggg cag ccc      466
43  Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly Gln Pro
44          5                   10                  15
46  aat gtc tcc tgc acg tgc aac tgc aaa cgc tct ttg ttc cag agc atg      514
47  Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln Ser Met
48          20                  25                  30
50  gag atc acg gag ctg gag ttt gtt cag atc atc atc atc gtg gtg gtg      562
51  Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val Val Val
52   35                   40                  45                  50
54  atg atg gtg atg gtg gtg gtg atc acg tgc ctg ctg agc cac tac aag      610
55  Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His Tyr Lys
56              55                      60                  65
58  ctg tct gca cgg tcc ttc atc agc cgg cac agc cag ggg cgg agg aga      658
59  Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg Arg
60              70                      75                  80
62  gaa gat gcc ctg tcc tca gaa gga tgc ctg tgg ccc tcg gag agc aca      706
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 63   Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr
 64             85                  90                  95
 66   gtg tca ggc aac gga atc cca gag ccg cag gtc tac gcc ccg cct cgg      754
 67   Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg
 68        100                 105                 110
 70   ccc acc gac cgc ctg gcc gtg ccg ccc ttc gcc cag cgg gag cgc ttc      802
 71   Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe
 72   115                 120                 125                 130
 74   cac cgc ttc cag ccc acc tat ccg tac ctg cag cac gag atc gac ctg      850
 75   His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu
 76                  135                 140                 145
 78   cca ccc acc atc tcg ctg tca gac ggg gag gag ccc cca ccc tac cag      898
 79   Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln
 80                  150                 155                 160
 82   ggc ccc tgc acc ctc cag ctt cgg gac ccc gag cag cag ctg gaa ctg      946
 83   Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu
 84             165                 170                 175
 86   aac cgg gag tcg gtg cgc gca ccc cca aac aga acc atc ttc gac agt      994
 87   Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser
 88        180                 185                 190
 90   gac ctg atg gat agt gcc agg ctg ggc ggc ccc tgc ccc ccc agc agt     1042
 91   Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser
 92   195                 200                 205                 210
 94   aac tcg ggc atc agc gcc acg tgc tac ggc agc ggc ggg cgc atg gag     1090
 95   Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu
 96                  215                 220                 225
 98   ggg ccg ccg ccc acc tac agc gag gtc atc ggc cac tac ccg ggg tcc     1138
 99   Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser
100                  230                 235                 240
102   tcc ttc cag cac cag cag agc agt ggg ccg ccc tcc ttg ctg gag ggg     1186
103   Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly
104             245                 250                 255
106   acc cgg ctc cac cac aca cac atc gcg ccc cta gag agc gca gcc atc     1234
107   Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile
108             260                 265                 270
110   tgg agc aaa gag aag gat aaa cag aaa gga cac cct ctc tagggtcccc      1283
111   Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
112   275                 280                 285
114   aggggggccg ggctggggct gcgtaggtga aaaggcag                          1321
116   <210> SEQ ID NO: 2
117   <211> LENGTH: 287
118   <212> TYPE: PRT
119   <213> ORGANISM: Homo Sapiens
121   <400> SEQUENCE: 2
122   Met His Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly
123    1               5                  10                  15
124   Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln
125             20                  25                  30
126   Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val
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127           35                    40                    45
128  Val Val Met Met Val Met Val Val Ile Thr Cys Leu Leu Ser His
129      50                    55                    60
130  Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg
131  65                    70                    75                    80
132  Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu
133                85                    90                    95
134  Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro
135            100                   105                   110
136  Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu
137            115                   120                   125
138  Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile
139      130                   135                   140
140  Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro
141  145                   150                   155                   160
142  Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu
143            165                   170                   175
144  Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe
145            180                   185                   190
146  Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro
147            195                  200                    205
148  Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg
149      210                   215                   220
150  Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro
151  225                   230                   235                   240
152  Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu
153            245                   250                   255
154  Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala
155      260                   265                   270
156  Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
157      275                   280                   285
159  <210> SEQ ID NO: 3
160  <211> LENGTH: 861
161  <212> TYPE: DNA
162  <213> ORGANISM: Homo Sapiens
164  <220> FEATURE:
165  <221> NAME/KEY: CDS
166  <222> LOCATION: (1)...(861)
168  <400> SEQUENCE: 3
169  atgcaccgct tgatgggggt caacagcacc gccgccgccg ccgccgggca gcccaatgtc      60
170  tcctgcacgt gcaactgcaa acgctctttg ttccagagca tggagatcac ggagctggag     120
171  tttgttcaga tcatcatcat cgtggtggtg atgatggtga tggtggtggt gatcacgtgc     180
172  ctgctgagcc actacaagct gtctgcacgg tccttcatca gccggcacag ccaggggcgg     240
173  aggagagaag atgccctgtc ctcagaagga tgcctgtggc cctcggagag cacagtgtca     300
174  ggcaacggaa tcccagagcc gcaggtctac gccccgcctc ggcccaccga ccgcctggcc     360
175  gtgccgccct cgcccagcg ggagcgcttc accgcttcc agcccaccta tccgtacctg     420
176  cagcacgaga tcgacctgcc acccaccatc tcgctgtcag acggggagga gcccccaccc     480
177  taccagggcc cctgcaccct ccagcttcgg accccgagc agcagctgga actgaaccgg     540
178  gagtcggtgc gcgcacccc aaacagaacc atcttcgaca gtgacctgat ggatagtgcc     600
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179  aggctgggcg gcccctgccc ccccagcagt aactcgggca tcagcgccac gtgctacggc     660
180  agcggcgggc gcatggaggg gccgccgccc acctacagcg aggtcatcgg ccactacccg     720
181  gggtcctcct tccagcacca gcagagcagt gggccgccct ccttgctgga ggggacccgg     780
182  ctccaccaca cacacatcgc gcccctagag agcgcagcca tctggagcaa agagaaggat     840
183  aaacagaaag gacaccctct c                                                861
185  <210> SEQ ID NO: 4
186  <211> LENGTH: 477
187  <212> TYPE: DNA
188  <213> ORGANISM: Homo Sapiens
190  <220> FEATURE:
191  <221> NAME/KEY: CDS
192  <222> LOCATION: (7)...(474)
193  <223> OTHER INFORMATION: IEX1
195  <400> SEQUENCE: 4
196  ctcacc atg tgt cac tct cgc agc tgc cac ccg acc atg acc atc ctg     48
197         Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu
198         1               5                   10
200  cag gcc ccg acc ccg gcc ccc tcc acc atc ccg gga ccc cgg cgg ggc     96
201  Gln Ala Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly
202   15                  20                  25                  30
204  tcc ggt cct gag atc ttc acc ttc gac cct ctc ccg gag ccc gca gcg     144
205  Ser Gly Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala
206                  35                  40                  45
208  gcc cct gcc ggg cgc ccc agc gcc tct cgc ggg cac cga aag cgc agc     192
209  Ala Pro Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser
210                  50                  55                  60
212  cgc agg gtt ctc tac cct cga gtg gtc cgg cgc cag ctg cca gtc gag     240
213  Arg Arg Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu
214              65                  70                  75
216  gaa ccg aac cca gcc aaa agg ctt ctc ttt ctg ctg ctc acc atc gtc     288
217  Glu Pro Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val
218          80                  85                  90
220  ttc tgc cag atc ctg atg gct gaa gag ggt gtg ccg gcg ccc ctg cct     336
221  Phe Cys Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro
222   95                  100                 105                 110
224  cca gag gac gcc cct aac gcc gca tcc ctg gcg ccc acc cct gtg tcc     384
225  Pro Glu Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser
226                  115                 120                 125
228  ccc gtc ctc gag ccc ttt aat ctg act tcg gag ccc tcg gac tac gct     432
229  Pro Val Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala
230                  130                 135                 140
232  ctg gac ctc agc act ttc ctc cag caa cac ccg gcc gcc ttc             474
233  Leu Asp Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe
234          145                 150                 155
236  taa                                                                  477
238  <210> SEQ ID NO: 5
239  <211> LENGTH: 156
240  <212> TYPE: PRT
241  <213> ORGANISM: Homo Sapiens
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243 <400> SEQUENCE: 5  .
244 Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu Gln Ala
245 1           5               10             15
246 Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly Ser Gly
247         20              25              30
248 Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala Ala Pro
249         35              40              45
250 Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser Arg Arg
251     50              55              60
252 Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu Glu Pro
253 65              70              75              80
254 Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val Phe Cys
255             85              90              95
256 Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro Pro Glu
257             100             105             110
258 Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser Pro Val
259         115             120             125
260 Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala Leu Asp
261     130             135             140
262 Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe
263 145             150             155
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 2704
267 <212> TYPE: DNA
268 <213> ORGANISM: Homo Sapiens
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (222)...(1394)
273 <223> OTHER INFORMATION: VDUP1
275 <400> SEQUENCE: 6
276 gcttagtgta accagcggcg tatatttttt aggcgccttt tcgaaaacct agtagttaat    60
277 attcatttgt ttaaatctta ttttattttt aagctcaaac tgcttaagaa taccttaatt   120
278 ccttaaagtg aaataatttt ttgcaaaggg gtttcctcga tttggagctt tttttttctt   180
279 ccaccgtcat ttctaactct taaaaccaac tcagttccat c atg gtg atg ttc aag   236
280                                               Met Val Met Phe Lys
281                                               1               5
283 aag atc aag tct ttt gag gtg gtc ttt aac gac cct gaa aag gtg tac   284
284 Lys Ile Lys Ser Phe Glu Val Val Phe Asn Asp Pro Glu Lys Val Tyr
285                 10              15              20
287 ggc agt ggc gag agg gtg gct ggc cgg gtg ata gtg gag gtg tgt gaa   332
288 Gly Ser Gly Glu Arg Val Ala Gly Arg Val Ile Val Glu Val Cys Glu
289             25              30              35
291 gtt act cgt gtc aaa gcc gtt agg atc ctg gct tgc gga gtg gct aaa   380
292 Val Thr Arg Val Lys Ala Val Arg Ile Leu Ala Cys Gly Val Ala Lys
293             40              45              50
295 gtg ctt tgg atg cag gga tcc cag cag tgc aaa cag act tcg gag tac   428
296 Val Leu Trp Met Gln Gly Ser Gln Gln Cys Lys Gln Thr Ser Glu Tyr
297     55              60              65
299 ctg cgc tat gaa gac acg ctt ctt ctg gaa gac cag cca aca ggt gag   476
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VERIFICATION SUMMARY   DATE: 10/17/2001
PATENT APPLICATION: US/09/934,249   TIME: 12:05:08

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10172001\I934249.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17